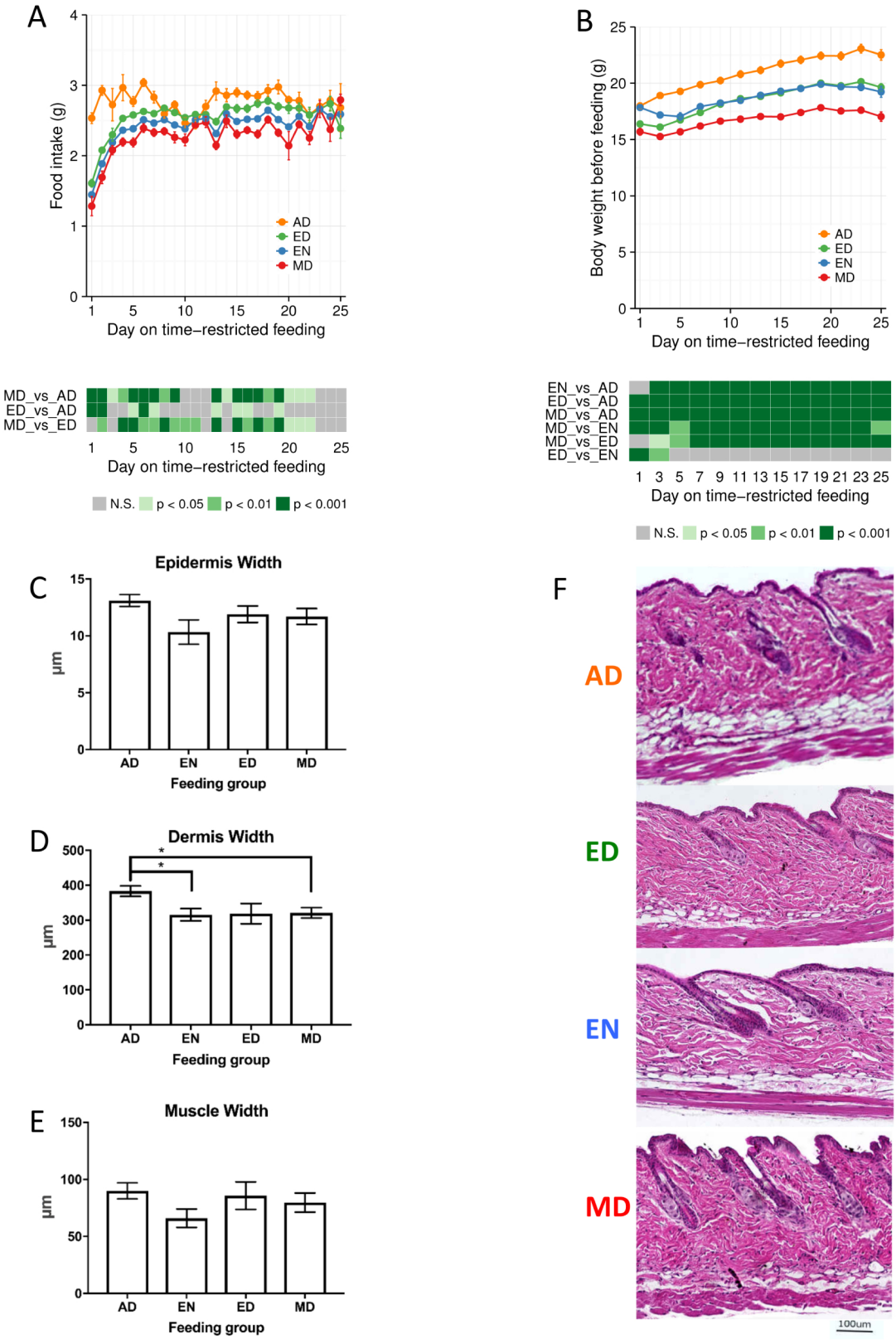


**Figure S1. Food intake, body weight, and skin histology after RF schedules, Related to Figure 1**

(A) Food intake throughout the RF protocol. Two-way ANOVA (Group × Time): RF schedule ($p < 0.001$), ZT time ($p < 0.001$) and RF schedule × ZT time ($p < 0.001$). Data are represented as mean ± SEM, N = 15-18. (B) Body weights throughout the RF protocol. Two-way ANOVA: RF schedule ($p < 0.001$), ZT Time ($p < 0.001$) and RF schedule × ZT time ($p < 0.001$). Data are represented as mean ± SEM, N = 11-36. For (A) and (B), Welch's t-test p-values comparing feeding groups at each timepoint are listed below the graphs. Shade of green indicates significance, with darker green being more significant. (C-E) Skin histology measurements. Skin was collected, paraffin embedded, sectioned and stained with hematoxylin and 20x mosaic images were acquired. The thickness of (C) epidermis, (D) dermis (including the intradermal fat layer), and (E) subcutaneous muscle were measured. Data is presented as Mean ± SEM for N=10-18 mice per group. Significance was determined by one-way ANOVA (only dermis showed significance with P= 0.03), followed by Student's paired t-test, shown as *$p < 0.05$. (F) Representative cropped images of skin histology from the RF groups quantified in C-E. 100 um scale bar is shown.

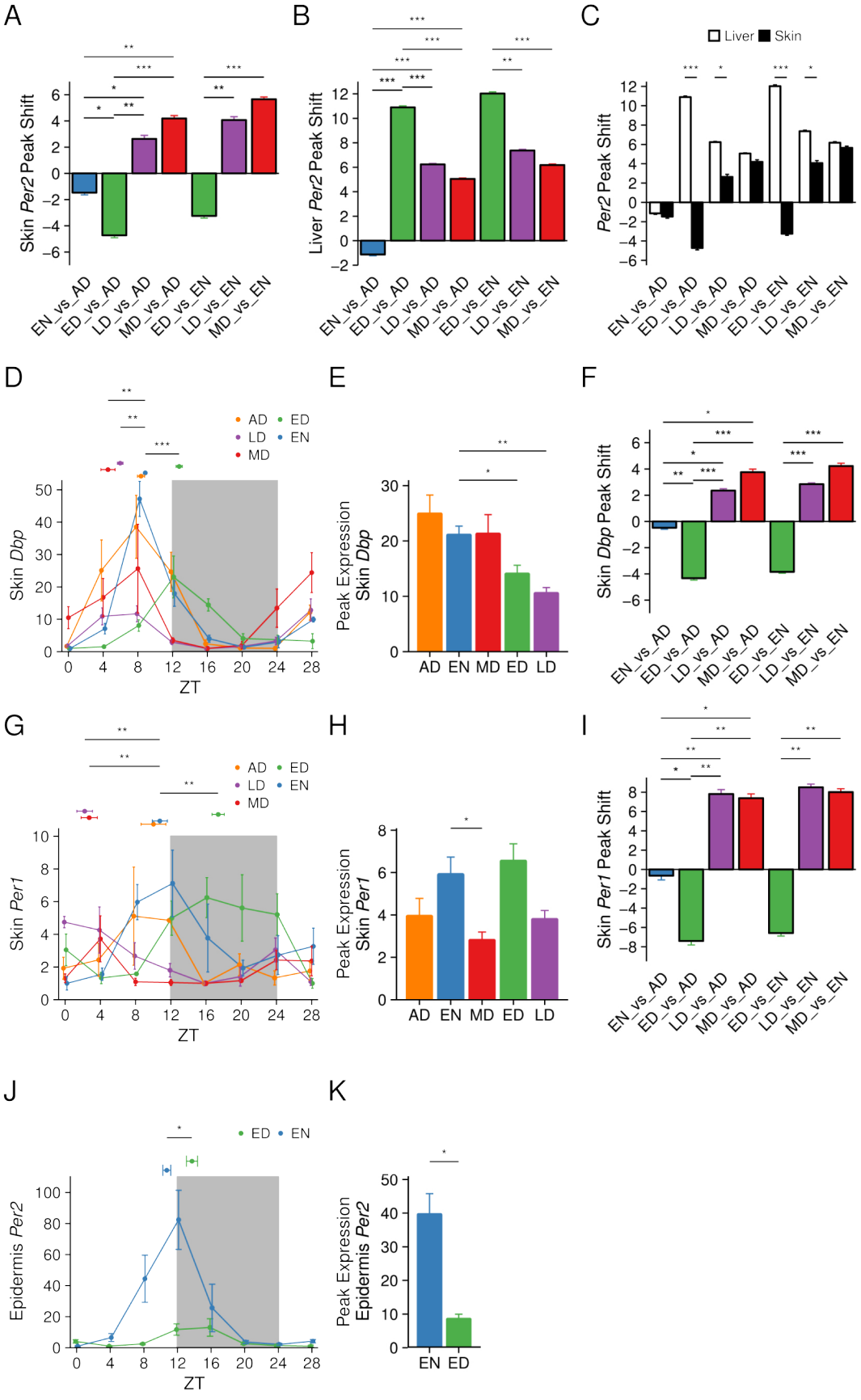


**Figure S2. *Per2*, *Dbp* and *Per1* expression and comparison of peak shifts, Related to Figure 1**

(*A*) Peak shift of skin *Per2* expression. (B) Peak shift of liver *Per2* expression. (C) Comparison of peak shifts of *Per2* expression in skin and liver. (D) *Dbp* gene expression in the skin measured by qPCR. (E) Peak expression of skin *Dbp*. (F) Comparison of the peak shifts of skin *Dbp* expression. (G) *Per1* gene expression in the skin measured by qPCR. (H) Peak expression of skin *Per1*. (I) Comparison of peak shifts of skin *Per1* expression. (J) *Per2* gene expression in the epidermis measured by qPCR. (K) Peak expression of epidermis *Per2*. (D, G, J) QPCR data is represented as mean ± SEM N = 3-5, after removal of outliers (Dixon's Q test, $Q_{99\%}$). The peak time of each group is shown above the curves represented as mean ± SEM N = 4. Watson-Williams test was used to compare the peak times (A-D, F, G, I, J) and Welch's t-test was used to peak expression levels (E, H, K). (A-K) For peak time and peak expression, the values represent mean ± SEM, N = 4. Statistical significance shown as *p < 0.05, **p < 0.01, *** p < 0.001.

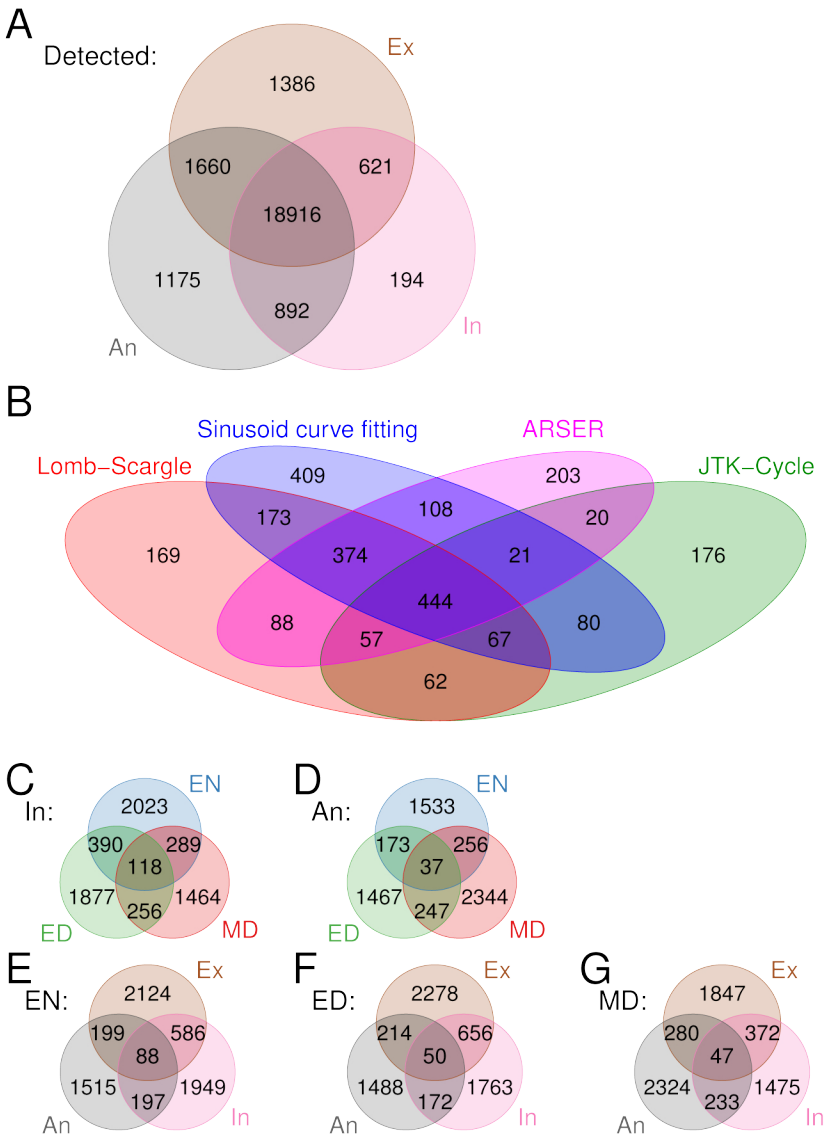


**Figure S3. Identification of diurnal transcripts, Related to Figure 2**

(A) Overlap of detected exons, introns and antisense transcripts. (B) Overlap of diurnal exons of EN identified by different algorithms. Genes identified as diurnal by any algorithm(s) are included. (C-D) Overlap of diurnal introns (C) and antisense (D) transcripts in three feeding groups. (E-G) Overlap of diurnal transcripts in EN (E), ED (F) and MD (G) (A and C-G) Ex: exons; An: antisense; In: introns.

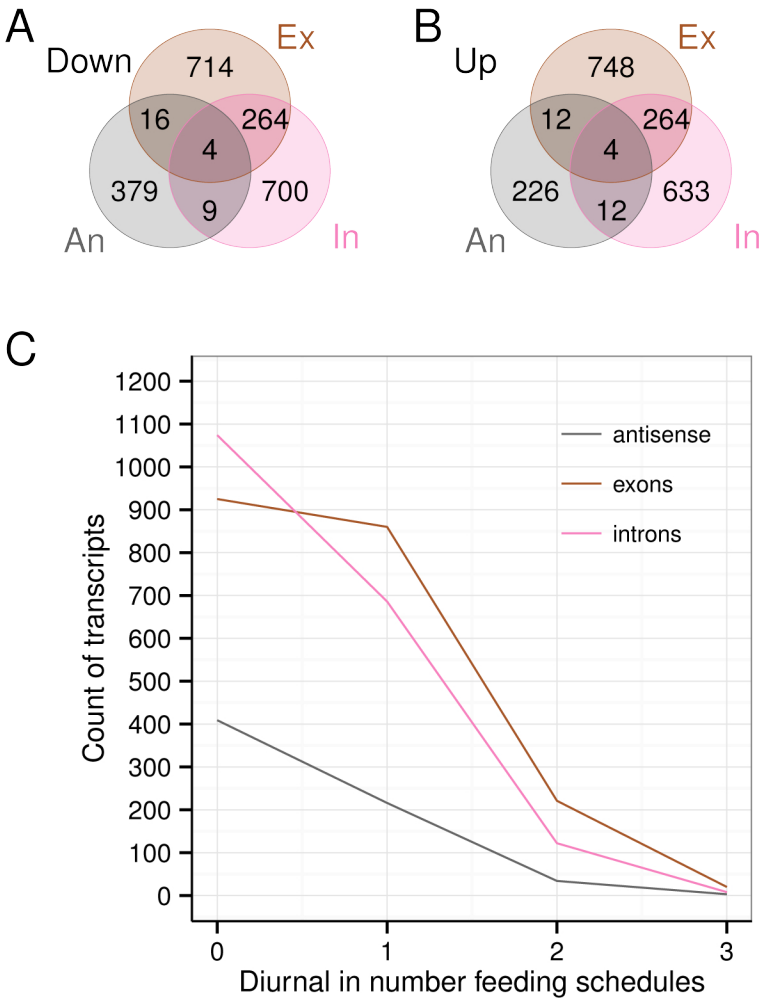


**Figure S4. Genes affected by food intake, Related to Figure 4**

(B) Overlap of transcripts upregulated after feeding. (A-B) Ex: exons; An: antisense; In: introns. (C) Graph depicting the number of feeding-affected transcripts that were identified as diurnal in 0, 1, 2, or 3 of the feeding groups.

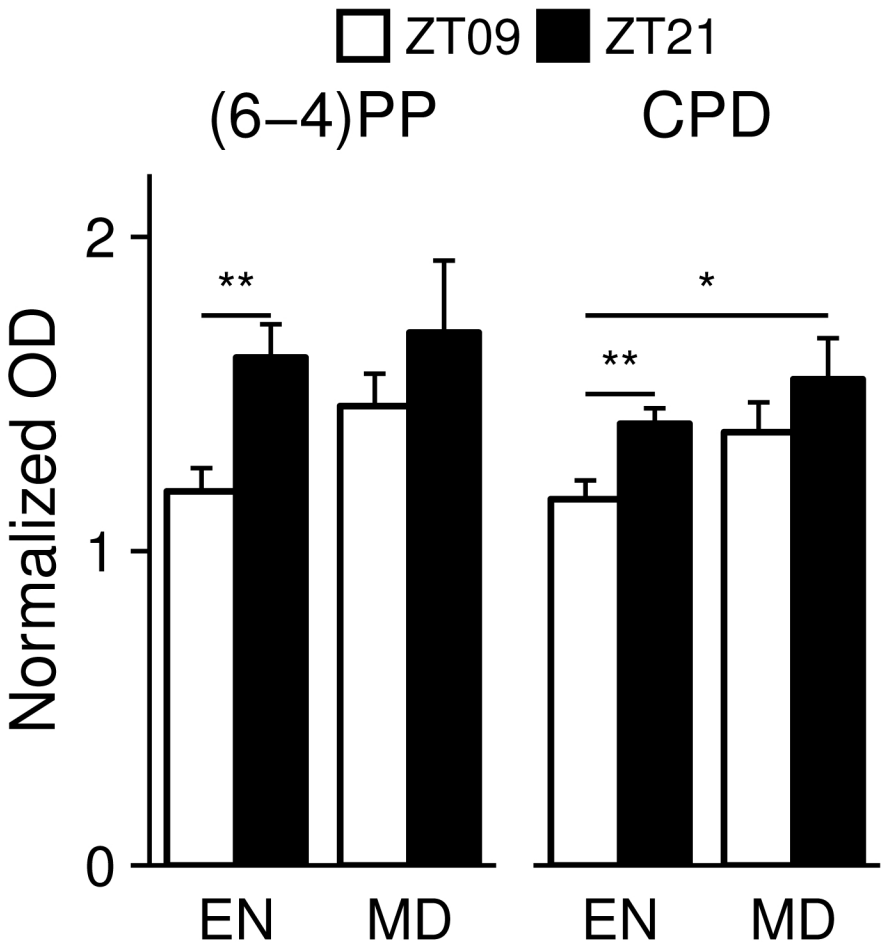


**Figure S5. Skin sensitivity to UVB-induced DNA damage, Related to Figure 6**

Quantification of (6-4)PP (left) and CPD (right) photoproducts after UVB exposure at ZT9 and ZT21 presented as Mean ± SEM (N = 8 or 9). Statistical significance comparing peak expression values was determined by Welch's t-test, shown as *$p < 0.05$, **$p < 0.01$, *** $p < 0.001$.

**Table S1. Sequencing statistics for the RNA-seq, Related to Figure 2**

Total reads, Mapped reads, percentage of reads mapped, non-rRNA reads, percentage of non-rRNA reads, reliable reads, and percentage of reliable reads, are indicated for RNA samples pooled from 2-4 mice per feeding group per time point as described in Methods section.

| RNA sample | | Total Reads | Mapped Reads | % | Non-rRNA Reads | % | Reliable Reads | % |
|---|---|---|---|---|---|---|---|---|
| MD | ZT0 | 53934987 | 50643956 | 94 | 47875030 | 89 | 43454124 | 81 |
| | ZT4 | 58618045 | 51192377 | 87 | 46375200 | 79 | 39297337 | 67 |
| | ZT8 | 63095384 | 52605332 | 83 | 44237151 | 70 | 33523750 | 53 |
| | ZT12 | 56033285 | 48428388 | 86 | 41704141 | 74 | 31765142 | 57 |
| | ZT16 | 59424906 | 52510958 | 88 | 46931580 | 79 | 38730040 | 65 |
| | ZT20 | 63122441 | 53106139 | 84 | 47206698 | 75 | 37788061 | 60 |
| | ZT24 | 58323439 | 51335336 | 88 | 47077225 | 81 | 41369525 | 71 |
| | ZT28 | 53651833 | 47565580 | 89 | 42935111 | 80 | 36460548 | 68 |
| ED | ZT0 | 64957607 | 56059860 | 86 | 50466217 | 78 | 39190824 | 60 |
| | ZT4 | 62418183 | 52613181 | 84 | 45941760 | 74 | 33349770 | 53 |
| | ZT8 | 63370673 | 53849389 | 85 | 46528867 | 73 | 32703877 | 52 |
| | ZT12 | 54188794 | 45372675 | 84 | 38868470 | 72 | 24701796 | 46 |
| | ZT16 | 59349340 | 47636646 | 80 | 41538428 | 70 | 27724999 | 47 |
| | ZT20 | 61264210 | 53695629 | 88 | 48245655 | 79 | 35409323 | 58 |
| | ZT24 | 53567052 | 45183962 | 84 | 39463990 | 74 | 25666218 | 48 |
| | ZT28 | 64239934 | 52534714 | 82 | 45068850 | 70 | 32519483 | 51 |
| EN | ZT0 | 63221149 | 50308240 | 80 | 43408139 | 69 | 28029993 | 44 |
| | ZT4 | 60383655 | 51373718 | 85 | 43435890 | 72 | 30094176 | 50 |
| | ZT8 | 62202466 | 53013034 | 85 | 46199673 | 74 | 31599842 | 51 |
| | ZT12 | 67298866 | 54763533 | 81 | 46887244 | 70 | 29689138 | 44 |
| | ZT16 | 59099629 | 47049092 | 80 | 39259630 | 66 | 25012802 | 42 |
| | ZT20 | 99558258 | 80519391 | 81 | 69863732 | 70 | 47313932 | 48 |
| | ZT24 | 59662234 | 47684780 | 80 | 40522893 | 68 | 27120354 | 45 |
| | ZT28 | 63367104 | 50211616 | 79 | 41047157 | 65 | 26751407 | 42 |